PCT09

```
        RAW SEQUENCE LISTING              DATE: 08/25/2003
        PATENT APPLICATION:  US/09/763,011C    TIME: 11:20:10

        Input Set : A:\CANDIDAamd2.txt
        Output Set: N:\CRF4\08252003\I763011C.raw
```

Does Not Comply
Corrected Diskette Needed

```
     5 <110> APPLICANT: Contreras, Roland
     6        Nelissen, Bart
     7        DeBacker, Marianne
     8        Luyten, Walter
     9        Viaene, Jasmine
    10        Logghe, Marc George
    13 <120> TITLE OF INVENTION: Drug Targets In Candida Albicans
    16 <130> FILE REFERENCE: 50899/002
C--> 19 <140> CURRENT APPLICATION NUMBER: US/09/763,011C
    21 <141> CURRENT FILING DATE: 2001-02-14
    24 <150> PRIOR APPLICATION NUMBER: 98310694.9
    26 <151> PRIOR FILING DATE: 1998-12-23
    29 <150> PRIOR APPLICATION NUMBER: 9817796.7
    31 <151> PRIOR FILING DATE: 1998-08-14
E--> 34 <160> NUMBER OF SEQ ID NOS: 114
    38 <170> SOFTWARE: PatentIn Ver. 2.0
```

114 is listed, but 123 sequence ID no's were counted. See page 4.

ERRORED SEQUENCES

```
    13547 <210> SEQ ID NO: 120
    13549 <211> LENGTH: 18
    13551 <212> TYPE: DNA
    13553 <213> ORGANISM: Artificial Sequence
    13555 <220> FEATURE:
    13557 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
    13560 <400> SEQUENCE: 120
E--> 13562 gcgtgaatgt aagcgtgac                                      18
```

Length listed as 18, but there are 19. See page 4.

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/25/2003
PATENT APPLICATION: US/09/763,011C   TIME: 11:20:12

Input Set : A:\CANDIDAamd2.txt
Output Set: N:\CRF4\08252003\I763011C.raw

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

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Seq#:1;  Line(s)  1,3,11,13,14,16,17,19,21,22,24,26,27,29,31,33,34,36,38,40
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/25/2003
PATENT APPLICATION: **US/09/763,011C**   TIME: 11:20:12

Input Set : **A:\CANDIDAamd2.txt**
Output Set: **N:\CRF4\08252003\I763011C.raw**

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Seq#:14;  Line(s)  1181,1183,1185,1187,1189,1191,1193,1195,1197,1199,1201
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VERIFICATION SUMMARY   DATE: 08/25/2003
PATENT APPLICATION: **US/09/763,011C**   TIME: 11:20:12

Input Set : **A:\CANDIDAamd2.txt**
Output Set: **N:\CRF4\08252003\I763011C.raw**

L:19 M:270 C: Current Application Number differs, Wrong Format
L:1081 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:48
M:341 Repeated in SeqNo=13
L:5761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:6720
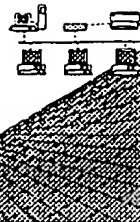L:6659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:2240
L:13368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:114 after pos.:416
M:341 Repeated in SeqNo=114
L:13562 M:254 E: No. of Bases conflict, LENGTH:Input:18 Counted:19 SEQ:120
L:13562 M:252 E: No. of Seq. differs, <211> LENGTH:Input:18 Found:19 SEQ:120
L:34 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (114) Counted (123)

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/763,011C_

Source: _PCT_

Date Processed by STIC: _08/25/2003_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
             Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/763011A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P

1_____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____ Variable Length.

Sequence(s)_____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7_____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000

9_✓_ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10_____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown is Artificial Sequence

11_____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (See 1.823 of Sequence Rules)

12_____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.